This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

Claims 1-24 (canceled)

Claim 25. (New) A method of assessing an individual's predisposition to a selected calcification condition status, which method comprises determining the genotype of the promoter of the bone sialoprotein gene (BSP II)- to determine whether the individual is homozygous or heterozygous for an allelic variation of the promoter of the bone sialoprotein gene, wherein said allelic variation is selected from (a) said promoter including the sequence

ATATAGAAGCCCAAG-**G**-AAAATCAGCTGACC (SEQ ID NO 18)
including guanine at the marked position rather than the sequence
ATATAGAAGCCCAAG-**A**-AAAATCAGCTGACC (SEQ ID NO 13)
including adenine at the marked position, said sequence occurring in said promoter at a position spanning approximately base pair 1496 of the sequence of said gene having GenBank accession number L24756
and (b) said promoter including the sequence
ATAGTGAAAACTTGT-**A**-TAATTATGAAATTTT (SEQ ID NO 19)
including adenine at the marked position rather than the sequence
ATAGTGAAAACTTGT-**G**-TAATTATGAAATTTT (SEQ ID NO 14)
including guanine at the marked position, said sequence occurring in said promoter at a position spanning approximately base pair 1869 of the sequence of said gene having GenBank accession number L24756,
and associating the presence of said adenine in said sequence spanning base pair 1496 bp with a predisposition to a lower peak bone mass and the presence of said guanine in said sequence spanning base pair 1869 bp with a predisposition to a lower peak bone mass.

Claim 26. (New) A method as claimed in Claim 25, which further comprises determining the genotype of the promoter of the matrix gla protein gene to determine whether the individual is homozygous or heterozygous for an allelic variation of the promoter of the matrix gla protein gene, wherein said allelic variation is said promoter including the sequence

TGGCTGGCTGGCTGG-**A**-TGGATGGATG (SEQ ID NO 20)

including adenine at the marked position rather than the sequence

TGGCTGGCTGGCTGG-**C**-TGGATGGATG (SEQ ID NO 15)

including cytosine at the marked position, said sequence occurring at a position spanning approximately base pair 242 of the sequence of said gene having GenBank accession number M55270, and associating the presence of said adenine in said sequence with a predisposition to a higher rate of loss of bone mass.

Claim 27. (New) A method as claimed in Claim 25, which further comprises determining the genotype of the promoter of the osteopontin gene to determine whether the individual is homozygous or heterozygous for an allelic variation of the promoter of the osteopontin gene, wherein said allelic variation is selected from (a) said promoter including the sequence

GTTTTTAGAATTTTC-**A**-GACTTCCCTCCACT (SEQ ID NO 21)

including adenine at the marked position rather than the sequence

GTTTTTAGAATTTTC-**G**-GACTTCCCTCCACT (SEQ ID NO 16)

including guanine at the marked position, said sequence occurring in the promoter at a position spanning approximately base pair 520 of the sequence of said gene having GenBank accession number D14813

and (b) said promoter including the sequence

GACAGAGGCAAGTT-**C**-TCTGAAGTCCTTGCA (SEQ ID NO 22)

including cytosine at the marked position rather than the sequence

GACAGAGGCAAGTT-**T**-TCTGAAGTCCTTGCA (SEQ ID NO 17)

including thymine at the marked position, said sequence occurring in the promoter at a

position spanning approximately base pair 1825 of the sequence of said gene having GenBank accession number D14813, and associating said adenine in the sequence spanning base pair 520 with a predisposition to a higher rate of loss of bone mass and the presence of said thymine in the sequence spanning base pair 1825 with a predisposition to a lower bone mass.

Claim 28. (New) A method as claimed in Claim 25, which further comprises determining the genotype of the promoter of the osteoprotegerin gene to determine whether the individual is homozygous or heterozygous for an allelic variation of the promoter of the osteoprotegerin gene, wherein said allelic variation is said promoter including the sequence
GACCAGGGAATT-**G**-ATGGGGGAGACAGCGAA (SEQ ID NO 23)
including guanine at the marked position rather than the sequence
GACCAGGGAATT-**A**-ATGGGGGAGACAGCGAA (SEQ ID NO 24)
including adenine at the marked position, said sequence occurring in the promoter at a position spanning approximately base pair 163 of the sequence of said gene having GenBank accession number AB008821, and associating the presence of said guanine in said sequence with a predisposition to a lower peak bone mass.

Claim 29. (New) A method as claimed in claim 25, comprising amplifying a relevant portion of the DNA of a said gene promoter of said individual.

Claims 30. (New) A method as claimed in Claim 29, wherein the sequence of said amplified portion is determined by hybridisation assay or by restriction fragment length analysis.